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Research Article

Morpho-phylogenetic evidence uncovers new taxa of lignicolous freshwater Sordariomycetes from Yunnan and Guizhou provinces, China

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Abstract

Lignicolous freshwater fungi play an important role in nutrient cycling and the maintenance of biodiversity within freshwater ecosystems. Recent intensive studies, particularly in Asia, have greatly advanced understanding of their taxonomy, diversity, and ecology. Yunnan and Guizhou provinces in southwestern China represent one of the most active regions for freshwater fungal research due to their complex topography, diverse freshwater bodies, and rich biodiversity. As part of a comprehensive investigation of lignicolous freshwater fungi in southwestern China, specimens were collected from rivers and plateau lakes. Multi-gene phylogenetic analyses based on a combined LSU, ITS, SSU, *rpb*2, and *tef*1-α dataset revealed that four monotypic genera, *Aquimonospora*, *Multiseptisporium*, *Paradiplococcium*, and *Platytrachelon*, form a distinct clade within Diaporthomycetidae families *incertae sedis* and are closely related to Melanascomaceae, Neodictyosporiaceae, Papulosaceae, and Pseudostanjehughesiaceae. Accordingly, a new family, Platytrachelaceae, is proposed to accommodate these genera. In addition, the genus *Multiseptisporium* is established to accommodate the type species *M. aquaticum* **sp. nov.**, which produces sporidesmium-like conidia. This study highlights the phylogenetic diversity and morphological complexity of sporidesmium-like taxa and underscores the importance of integrating morphological and phylogenetic evidence to resolve their taxonomic relationships. The findings enrich the known diversity of lignicolous freshwater fungi in Yunnan and Guizhou and provide new insights into their taxonomy and ecological adaptation within freshwater ecosystems.

Key words: Lignicolous freshwater fungi, Platytrachelaceae, taxonomy, Yunnan–Guizhou Plateau

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Introduction

Lignicolous freshwater fungi are those colonizing woody substrates in a variety of freshwater habitats, including lentic habitats (such as lakes, ponds, and reservoirs), lotic habitats (such as rivers and streams), and artificial habitats (such as water-cooling towers) (Luo et al. 2004; Hyde et al. 2016; Calabon et al. 2022, 2023). As saprophytes, they play a crucial role in the decomposition of lignocellulosic material and the release of nutrients, thus contributing to the maintenance of biodiversity in freshwater ecosystems (Yuen et al. 1998; Bucher et al. 2004; Hyde et al. 2016). Lignicolous freshwater fungi have been the subject of extensive research globally and within Asia, particularly in China and Thailand, which have emerged as major centers of study (Zhang et al. 2011; Jones et al. 2014; Hyde et al. 2016, 2021; Su et al. 2016; Bao et al. 2018, 2019, 2020, 2021, 2023; Luo et al. 2018a, 2019; Dong et al. 2020, 2021a, b; Calabon et al. 2021, 2022, 2023; Shen et al. 2022a, b, 2024a; Fryar and Catcheside 2023; Fryar et al. 2023; Xu et al. 2023, 2024, 2025a; Yang et al. 2023; Wang et al. 2024a, b; Xiao et al. 2025). Significant advances in this field have been made through the concerted efforts of prominent research institutions such as the Center of Excellence in Fungal Research (Mae Fah Luang University), Chiang Mai University, the University of Hong Kong, Dali University, and the Kunming Institute of Botany, Chinese Academy of Sciences (KIB-CAS). Through the integration of detailed morphological characterization and multi-gene phylogenetic analyses, researchers have successfully discovered numerous novel species from diverse freshwater habitats (Su et al. 2016; Luo et al. 2019; Dong et al. 2020, 2021a; Calabon et al. 2021, 2022; Hyde et al. 2021; Bao et al. 2023; Yang et al. 2023; Shen et al. 2024a; Wang et al. 2024b). Among the regions contributing significantly to this progress, Yunnan and Guizhou provinces in southwestern China stand out as the most active and productive areas for freshwater fungal research, with numerous species documented from streams, rivers, and lakes (Cai et al. 2002; Luo et al. 2016, 2017, 2018a, b, 2019; Su et al. 2016; Bao et al. 2018, 2020, 2023; Dong et al. 2020, 2021b; Yang et al. 2021, 2023; Du et al. 2022; Shen et al. 2022a, b, 2023, 2024a, b; Shen and Luo 2023; Xu et al. 2023; Ma et al. 2024; Wang et al. 2024a, b; Liu et al. 2025).

Sordariomycetes is one of the largest and most ecologically diverse classes within the phylum Ascomycota, comprising numerous lineages that inhabit a wide range of terrestrial and aquatic ecosystems (Maharachchikumbura et al. 2015; Luo et al. 2019; Hyde et al. 2020, 2021; Huang et al. 2021; Bao et al. 2023). Among these, lignicolous freshwater fungi within Sordariomycetes represent a highly diverse and ecologically important group (Luo et al. 2019; Hyde et al. 2020, 2021; Bao et al. 2023; Yang et al. 2023). In recent years, intensive studies focusing on this group have greatly expanded our understanding of its taxonomic diversity, distribution patterns, and ecological significance in freshwater environments (Luo et al. 2019; Hyde et al. 2020, 2021; Calabon et al. 2021; Dong et al. 2021b; Bao et al. 2023; Yang et al. 2023). These investigations have led to the discovery and description of numerous new species, highlighting the hidden diversity of freshwater Sordariomycetes. Lignicolous freshwater species of Sordariomycetes are primarily assigned to orders such as Annulatascales, Chaetosphaeriales, Distoseptisporales, Hypocreales, Microascales, Pleurotheciales, Savoryellales, Sporidesmiales,

and Diaporthomycetidae families *incertae sedis* (Luo et al. 2019; Réblová et al. 2020a, b; Dong et al. 2021a, b; Li et al. 2021; Yang et al. 2021, 2023; Calabon et al. 2022; Zhang et al. 2022; Bao et al. 2023; Yu et al. 2023; Wang et al. 2025b).

Many species within the class Sordariomycetes exhibit highly similar morphological characteristics, which pose significant challenges to traditional taxonomy that relies solely on morphology. Limited diagnostic features and overlapping characters often confound taxonomists, making it difficult to distinguish closely related taxa with sufficient confidence (Bhunjun et al. 2021; Jayawardena et al. 2021; Maharachchikumbura et al. 2021; Chen et al. 2023; Dissanayake et al. 2024). For example, some endophytic and pathogenic fungi, along with certain saprophytic taxa such as species of *Apiospora*, *Colletotrichum*, *Diaporthe*, *Fusarium*, chloridium-like taxa, and sporidesmium-like taxa, share remarkably similar morphological characteristics (Crous and Groenewald 2013; Su et al. 2016; Crous et al. 2021; Jayawardena et al. 2021; Koukol and Delgado 2021; Pintos and Alvarado 2021; Talhinhas and Baroncelli 2021; Monkai et al. 2022; Norphanphoun et al. 2022; Réblová et al. 2022; Réblová and Nekvindová 2023; Delgado et al. 2024; Dissanayake et al. 2024). These morphological similarities make it nearly impossible to achieve precise species delimitation through morphology alone (Bhunjun et al. 2021; Jayawardena et al. 2021; Maharachchikumbura et al. 2021; Chen et al. 2023; Dissanayake et al. 2024).

To overcome these limitations, the application of multi-gene phylogenetic analyses in conjunction with detailed morphological assessments has proven to be a powerful and indispensable approach. This integrative method has greatly enhanced the resolution of species boundaries and enabled the discovery of cryptic diversity within morphologically conserved groups (Bhunjun et al. 2021; Jayawardena et al. 2021; Maharachchikumbura et al. 2021; Chen et al. 2023; Dissanayake et al. 2024). Through comprehensive re-evaluation using both multi-gene phylogenetic analyses and morphological evidence, several underestimated or misclassified taxa have been correctly re-identified and newly described, contributing to a more accurate and refined classification framework for the group (Crous et al. 2021; Hyde et al. 2021; Jayawardena et al. 2021; Pintos and Alvarado 2021; Talhinhas and Baroncelli 2021; Réblová et al. 2022; Wu and Diao 2022; Bao et al. 2023; Réblová and Nekvindová 2023; Delgado et al. 2024; Dissanayake et al. 2024).

At present, we are undertaking a systematic and comprehensive investigation of the diversity and ecology of lignicolous freshwater fungi in southwestern China (Shen et al. 2022b, 2024a; Shen and Luo 2023; Wang et al. 2025a). These research programs encompass a wide array of freshwater habitats, including major rivers, tributaries, plateau lakes, and micro-water bodies in alpine regions. The sampling efforts span both internationally and nationally significant drainage basins, aiming to capture the ecological and taxonomic diversity of fungi associated with submerged woody substrates. In this study, lignicolous freshwater fungi were collected from a river and a plateau lake in Guizhou and Yunnan provinces. Through detailed morphological examinations combined with multi-gene phylogenetic analyses, three novel taxa were identified and are formally introduced in this paper. This study not only increases the known species richness of freshwater wood-inhabiting fungi in Yunnan but also enhances broader understanding of their distribution and phylogenetic relationships. The results underscore the

importance of integrated taxonomic approaches in uncovering cryptic fungal diversity, particularly in underexplored and ecologically diverse regions such as international rivers, tributaries, plateau lakes, and micro-water bodies.

Materials and methods

Specimen collection, examination, and isolation

Specimens of submerged decaying wood were collected from Yilonghu Lake (Yunnan Province) in spring and from a stream (Guizhou Province) in autumn. The samples were brought to the laboratory and incubated in sterile, damp plastic boxes at room temperature for one week. Morphological observations were conducted following the methods of Shen et al. (2023). Macro-morphological characteristics of the samples were observed using an Optec SZ 760 compound stereomicroscope (Chongqing Optec Instrument Co., Ltd., Chongqing, China). Temporarily mounted microscope slides were examined and photographed under a Nikon ECLIPSE Ni-U compound stereomicroscope (Nikon, Tokyo, Japan). The morphological characteristics of colonies on their natural substrates were documented using a Nikon SMZ1000 stereo zoom microscope (Nikon, Tokyo, Japan). Photomicrograph measurements were performed using Tarosoft® Image Framework version 0.9.7. Image processing and layout adjustments were conducted using Adobe Photoshop CS5 Extended version 12.0.0.0 (Adobe Systems Inc., San Jose, CA, USA).

Single-spore isolations were carried out based on the method described by Shen et al. (2023). Germinated conidia were individually transferred to fresh potato dextrose agar plates (PDA; Beijing Bridge Technology Co., Ltd., Beijing, China) and incubated at ambient room temperature under alternating dark and light conditions to promote colony development and sporulation. To document the origin and development of germ tubes, germinated spores along with the surrounding agar were mounted in sterile water on glass slides and photographed under a microscope. Following microscopic observation and isolation, the fungal specimens were air-dried under ambient conditions, wrapped in absorbent paper, and sealed in zip-lock plastic bags with mothballs for long-term preservation. Voucher specimens were deposited in the Herbarium of the Kunming Institute of Botany, Chinese Academy of Sciences (**HKAS**), Kunming, China, and the Herbarium of the Guizhou Academy of Agricultural Sciences (**GZAAS**), Guiyang, China. Living cultures were deposited in the Kunming Institute of Botany Culture Collection (**KUNCC**), Kunming, China, and the Guizhou Culture Collection (**GZCC**), Guiyang, China. Fungal Names numbers were registered in the Fungal Names database (https://nmdc.cn/fungalnames/registe; accessed on 4 October 2025; Wang et al. 2023).

DNA extraction, PCR amplification, and sequencing

DNA extraction, PCR amplification, sequencing, and phylogenetic analyses were carried out following the methods described by Dissanayake et al. (2020). Mycelia used for DNA extraction were cultivated on PDA for 3–4 weeks at 24 °C. From each isolate, total genomic DNA was extracted from 100–150 mg of axenic mycelium, which was carefully scraped from the edges of the growing culture with a sterile scalpel. The material was transferred to a 1.5 mL microcentrifuge

tube using sterilized inoculum needles. Mycelium was ground to a fine powder with liquid nitrogen or quartz sand to disrupt the cells for DNA extraction. DNA was extracted using the Trelief™ Plant Genomic DNA Kit (TSP101) following the manufacturer's guidelines (Beijing Tsingke Biological Engineering Technology and Services Co., Ltd., Beijing, P.R. China).

Polymerase chain reaction (PCR) amplification was performed following the protocol described by Shen et al. (2024b), and the thermal cycling conditions are shown in Table 1. Five gene regions, internal transcribed spacer (ITS), large subunit ribosomal RNA (LSU), small subunit ribosomal RNA (SSU), translation elongation factor 1-alpha (*tef*1-α), and the second largest subunit of RNA polymerase II (*rpb*2), were amplified using the primer pairs ITS5/ITS4 (White et al. 1990), LR0R/LR7 (Vilgalys and Hester 1990), NS1/NS4 (White et al. 1990), EF1-983F/EF1-2218R (Liu et al. 1999), and RPB2-5F/RPB2-7cR (Liu et al. 1999), respectively. PCR products were purified using minicolumns, purification resin, and buffer according to the manufacturer's protocols. Sequencing of purified PCR amplicons was performed by Beijing Tsingke Biological Engineering Technology and Services Co., Ltd. (Beijing, P.R. China).

Phylogenetic analysis

BLAST searches were conducted using the BLASTn algorithm to retrieve closely related sequences from GenBank (http://www.ncbi.nlm.nih.gov). Multiple sequence alignments were performed using the MAFFT online service (version 7) with default settings (Kuraku et al. 2013; Katoh et al. 2019; http://mafft.cbrc.jp/alignment/server/index.html, accessed on 20 September 2025), and poorly aligned regions were trimmed using trimAl version 1.2 with default parameters (http://trimal.cgenomics.org for specific operation steps; Capella-Gutiérrez et al. 2009). Aligned sequences from different loci were concatenated using SequenceMatrix v1.7.8 (Vaidya et al. 2011). The resulting concatenated dataset in FASTA format was converted into PHYLIP and NEXUS formats using the ALignment Transformation EnviRonment (ALTER) online platform (http://sing.ei.uvigo.es/ALTER/, accessed on 20 September 2025).

Phylogenetic analyses were performed using both maximum likelihood (ML) and Bayesian inference (BI) approaches. ML analysis was performed using RAxML-HPC2 on XSEDE (8.2.12) (Stamatakis 2006; Stamatakis et al. 2008) in the CIPRES Science Gateway (Miller et al. 2010; http://www.phylo.org/portal2; accessed on 20 September 2025), applying the GTR+GAMMA model with 1,000 bootstrap replicates. Bayesian analysis was implemented in MrBayes version 3.2.6 (Ronquist et al. 2012), with the best-fit model of nucleotide substitution determined using MrModeltest 2.2 (Guindon and Gascuel 2003; Darriba et al.

Table 1. PCR thermocycling conditions for genes used in this paper.

Genes	Initial denaturation		Denaturation		Annealing		Extension		Final extension		No. of cycles
	Temp (°C)	Time (min)	Temp (°C)	Time (s)	Temp (°C)	Time (s)	Temp (°C)	Time (s)	Temp (°C)	Time (min)	
ITS, SSU	94	3	94	30	56	50	72	60	72	10	30
LSU	94	3	94	50	55	60	72	60	72	10	30
*tef*1-α	94	3	94	50	55	60	72	60	72	10	30
*rpb*2	94	5	94	60	52	90	72	90	72	10	38

2012). Posterior probabilities (PP) were estimated using a Markov chain Monte Carlo (MCMC) sampling approach (Rannala and Yang 1996). Six simultaneous Markov chains were run for 20,000,000 generations, with trees sampled every 1,000 generations, and the first 25% of trees discarded as burn-in.

Phylogenetic trees were visualized using FigTree v1.4.4 (http://tree.bio.ed.ac.uk/software/figtree) and subsequently edited and formatted for publication using Adobe Illustrator (Adobe Systems Inc., San Jose, CA, USA). Newly generated sequences were deposited in GenBank, and detailed strain information, including accession numbers and voucher data, is provided in Table 2. The alignments and phylogenetic trees were deposited in TreeBASE (http://www.treebase.org/, accession number 32456).

Table 2. Taxa used in the phylogenetic analyses and their corresponding GenBank accession numbers. Notes: The ex-type cultures are indicated using "T" after strain numbers; newly generated sequences are indicated in bold. A hyphen (–) stands for no sequence data in GenBank.

Taxon	Source	GenBank accession numbers				
		ITS	LSU	SSU	*rpb2*	*tef1-α*
Achroceratosphaeria potamia	CBS 125414 T	MH863679	GQ996538	GQ996541	KM588908	–
Acrodictys bawanglingensis	SAUCC 1342 T	ON606324	ON614219	ON620164	ON859853	–
Acrodictys chishuiensis	GZCC 20-0513 T	OP377810	OP377909	OP377995	OP473084	–
Afroraffaelea ambrosiae	CBS 141678 T	OM632703	OM584293	–	OM631577	–
Annulatascus tratensis	MFLUCC 17-2055 T	OP377891	OP377977	OP378052	–	–
Annulatascus velatisporus	MFLUCC 16-1441	KY320183	KY244031	KY244032	–	–
Aquapteridospora hyalina	GZCC 22-0072T	ON527937	ON527945	–	ON533689	ON533681
Aquapteridospora jiangxiensis	JAUCC 3008 T	MZ871501	MZ871502	–	MZ855768	MZ855767
Aquimonospora tratensis	MFLUCC 17-2133 T	MK335798	MK335797	MK335778	MK344654	–
Ascolacicola aquatica	CGMCC 3.27466	PQ644539	PQ650108	PQ844522	PQ824476	PQ824490
Ascolacicola minispora	KUNCC 23-14565 T	OR589283	OR600931	OR743193	OR820903	OR739157
Ascotaiwania lignicola	NIL 00005	HQ446341	HQ446364	HQ446284	HQ446419	HQ446307
Atractospora thailandensis	KUMCC 16-0067 T	MF374353	MF374362	MF374371	MF370951	MF370962
Bactrodesmium diversum	CBS 144081 T	MN699356	MN699416	MN699372	MN704295	MN704320
Bactrodesmium obovatum	CBS 144077	MN699395	MN699424	MN699375	MN704298	MN704322
Barbatosphaeria arboricola	CBS 127689 T	MH864681	MH876117	KM492849	KM492901	–
Barbatosphaeria hippocrepida	ICMP 17630 T	KM492894	FJ617557	HQ878599	HQ878608	–
Barbatosphaeria varioseptata	CBS 137797 T	KM492896	KM492869	KM492857	KM492907	–
Barrmaelia macrospora	CBS 142768 T	KC774566	KC774566	–	MF488995	MF489005
Barrmaelia moravica	CBS 142769 T	MF488987	MF488987	–	MF488996	MF489006
Bullimyces communis	AF281-5	–	JF775587	JF758619	–	–
Cancellidium cinereum	MFLUCC 18-0424 T	MT370353	MT370363	MT370351	MT370486	MT370488
Cancellidium griseonigrum	MFLUCC 17-2117 T	MT370354	MT370364	MT370352	MT370487	–
Ceratolenta caudata	CBS 125234 T	–	JX066704	JX066708	JX066699	–
Ceratosphaeria aquatica	MFLUCC 18-1337 T	MK828612	MK835812	–	MN156509	MN194065
Ceratosphaeria lignicola	MFLUCC 18-0342	MK828613	MK835813	–	–	MN194066
Ceratostomella melanospora	CBS 147993 T	PQ215757	PQ215750	PQ215925	PQ213491	PQ213502
Ceratostomella pyrenaica	CBS 117116 T	PQ215759	DQ076323	DQ076324	PQ213492	PQ213503
Ceratostomella sordida	CBS 116000	PQ215761	AY761087	AY761090	KY931929	PQ213505
Chloridiopsiella preussii	CBS 230.75 T	OR134700	OR134645	–	OR135580	OR130780
Chloridiopsis constrictospora	CBS 432.92 T	OR134704	OR134649	–	OR135584	OR130784
Chlorociboria aeruginosa	AFTOL-ID 151	DQ491501	AY544669	–	DQ470886	DQ471053
Conlarium baiseense	HMAS 247298 T	MF083157	MF083158	MF083159	MK573000	–

Taxon	Source	GenBank accession numbers				
		ITS	LSU	SSU	*rpb2*	*tef1-α*
Conlarium nanningense	HMAS 247075 T	KX886204	KX886202	KX886203	MK572998	–
Corollospora fusca	NBRC 32107	JN943382	JN941483	JN941662	–	–
Corollospora gracilis	NBRC 32111	JN943386	JN941487	JN941659	–	–
Dermea acerina	AFTOL-ID 941	MH855942	DQ247801	DQ247809	DQ247791	DQ471091
Diaporthostoma machili	CFCC 52100 T	MG682080	MG682020	–	MG682040	–
Diaporthostoma machili	CFCC 52101 T	MG682081	MG682021	–	MG682041	–
Diluviicola aquatica	MFLUCC 15-0986 T	MF374356	MF374365	–	MF370953	MF370961
Distoseptispora bambusae	MFLUCC 20-0091	MT232713	MT232718	MT232716	MT232881	MT232880
Distoseptispora palmarum	MFLUCC 18-1446	MK085062	MK079663	MK079661	MK087670	MK087660
Entosordaria perfidiosa	CBS 142773 T	MF488993	MF488993	–	MF489003	MF489012
Entosordaria quercina	CBS 142774 T	MF488994	MF488994	–	MF489004	MF489013
Fluminicola aquatica	MFLU 15-2710 T	MF374357	MF374366	MF374374	–	MF370960
Fluminicola saprophytica	MFLUCC 15-0976 T	MF374358	MF374367	MF374375	MF370954	MF370956
Fluminicola striata	MFLUCC 18-0990 T	MW286496	MW287770	–	–	–
Graphilbum crescericum	CBS 130864 T	OM501403	OM514749	–	OM631604	–
Hawksworthiomyces crousii	MUCL55928 T	KX396551	KX396548	–	OM631609	–
Jobellisia fraterna	SMH 2863	–	AY346285	–	–	–
Jobellisia guangdongensis	HMAS 251240 T	NR_138381	NG_068733	–	–	–
Lentomitella magna	ICMP 18371 T	KY931786	KY931815	KY931871	KY931843	–
Lindriella thalassiae	AFTOL ID 413	DQ491508	DQ470947	DQ470994	FJ238382	DQ471065
Lulworthia atlantica	FCUL061107CP3	KT347208	JN886825	KT347196	–	OQ296422
Lulworthia norwegica	TRä3123A	OP683562	OP648294	OP680778	OP715904	OP715908
Melanascoma panespora	AD291710 T	–	OQ789909	–	–	–
Melanascoma panespora	AD219607	–	OQ799385	–	–	OQ870569
Myrmecridium hydei	MFLUCC 23-0217 T	OR500543	OR500545	–	OR515019	OR515020
Neodictyosporium cheirosporum	CGMCC 3.27450 T	PQ067912	PQ067743	PQ066579	–	PQ271578
Neodictyosporium cheirosporum	UESTCC 24.0121 T	PQ067906	PQ067737	PQ066573	PQ241075	PQ271577
Neodictyosporium sexuale	CGMCC 3.27441 T	PQ067893	PQ067724	PQ066563	PQ241074	PQ271583
Neodictyosporium sexuale	UESTCC 24.0112 T	PQ067892	PQ067723	PQ066562	PQ241073	–
Neomyrmecridium aquaticum	S-1158	MK828656	MK849803	MK828322	MN124540	MN194061
Nigroconidius bambusae	CGMCC 3.27446 T	PQ067898	PQ067729	PQ066566	PQ247602	PQ280792
Nigroconidius bambusae	UESTCC 24.0160	PQ067909	PQ067739	PQ066575	PQ247603	PQ280793
Nigroconidius septatus	CGMCC 3.27449 T	PQ067905	PQ067736	PQ066572	PQ247605	PQ280797
Nigroconidius septatus	UESTCC 24.0162	PQ067904	PQ067733	PQ066570	PQ247606	PQ280795
Ophioceras dolichostomum	CBS 114926	JX134677	JX134689	JX134663	–	JX134703
Ophioceras thailandense	MFLUCC 15-0603 T	OP377882	OP377968	OP378045	–	OP473057
Papulosa amerospora	AFTOL ID 748	–	DQ470950	DQ470998	DQ470901	DQ471069
Paradiplococcium singulare	FMR 10752 T	KY853456	KY853517	–	–	–
Paralulworthia gigaspora	MUT 5086	MZ357716	MZ357738	MZ357759	MZ357221	MZ407522
Paraproliferophorum hyphaenes	CPC 40103 T	ON603770	ON603790	–	–	ON605632
Pararamichloridium caricicola	CBS 145069 T	MK047438	MK047488	–	–	–
Pararamichloridium verrucosa	CBS 128.86 T	MH861933	MH873621	NG_065540	–	–
Multiseptisporium aquaticum	**KUNCC 23-14304 T**	**PX230562**	**PX230548**	**–**	**PX238393**	**PX238386**
Multiseptisporium aquaticum	**GZCC 24-0036**	**PX230563**	**PX230549**	**PX230534**	**PX238394**	**PX238387**
Perennicordyceps cuboidea	NBRC 103836	JN943332	JN941420	JN941721	AB972955	AB972951
Perennicordyceps paracuboidea	NBRC 100942	JN943337	JN941430	JN941711	AB972958	AB972954
Phaeoacremonium novae-zealandiae	CBS 110156 T	MH862854	NG_068987	NG_062040	–	–
Phaeoacremonium rubrigenum	CBS 498.94 T	MH862477	MH874125	–	–	–
Phomatospora bellaminuta	AFTOL-ID 766	–	FJ176857	–	FJ238345	–

Taxon	Source	GenBank accession numbers				
		ITS	LSU	SSU	*rpb2*	*tef1-α*
Phomatospora uniseriata	MFLUCC 17-2068 T	MT310660	MT214616	MT226727	MT394720	MT394672
Pisorisporium cymbiforme	PRM 924378	–	KM588902	KM588899	KM588905	–
Pisorisporium cymbiforme	PRM 924379	–	KM588903	KM588900	KM588906	–
Pisorisporium cymbiforme	CBS 138884	–	KM588904	KM588901	KM588907	–
Platytrachelon abietis	CBS 125235 T	–	NG_057957	NG_061135	JX066698	–
Pleurostoma ootheca	CBS 115329 T	HQ878590	AY761079	AY761074	HQ878606	–
Pleurostoma richardsiae	CBS 270.33 T	AY179948	AB364684	AY761066	HQ878607	–
Proliferophorum thailandicum	MFLUCC 17-0293	MK028344	MK028343	MK028345	–	–
Pseudodactylaria longidenticulata	MFLUCC 17-2383 T	OP377857	OP377942	OP378023	OP473102	OP473036
Pseudodactylaria uniseptata	MFLUCC 17-2395 T	OP377892	OP377978	OP378053	OP473122	OP473063
Pseudohalonectria aurantiaca	MFLUCC 15-0379 T	OP377881	OP377967	OP378044	–	OP473056
Pseudohalonectria hampshirensis	isolate 168	–	KX426220	KX426222	–	KX426225
Pseudohalonectria hampshirensis	isolate 177	–	KX426218	KX426221	–	KX426224
Pseudomelanconis caryae	CFCC 52110 T	MG682082	NG_067555	–	MG682042	–
Pseudomelanconis caryae	CFCC 52112 T	MG682084	MG682024	–	MG682044	–
Pseudoplagiostoma alsophilae	SAUCC WZ0451 T	OP810625	OP810631	–	OP828578	–
Pseudoplagiostoma altingiae	CGMCC 3.28244 T	PQ338993	PQ339638	–	PQ367345	–
Pseudoproboscispora thailandensis	MFLUCC 15-0989 T	MF374360	MF374369	MF374377	–	MF370959
Pseudostanjehughesia aquitropica	MFLUCC 16-0569 T	MF077548	MF077559	MF077537	–	MF135655
Pseudostanjehughesia hydei	KUNCC 23-14302	PQ845936	PX245755	PX218427	PX233791	PX238285
Pseudostanjehughesia hydei	KUNCC 23-14310 T	PQ845937	PX245756	PX218428	PX233792	PX238286
Pseudostanjehughesia lignicola	MFLUCC 15-0352 T	MK828643	MK849787	–	MN124534	MN194047
Pseudostanjehughesia nielamuensis	KUNCC 10407 T	OP626330	PQ152658	PQ218305	PV657977	PV525047
Pseudostanjehughesia nielamuensis	KUNCC 24-18109	PQ168269	PQ152659	PQ218306	PV657978	PV525048
Pseudothailandiomyces nypae	MFLUCC 24-019 T	–	PP621108	PP639237	PP780199	PP761025
Rhamphoria delicatula	MR1396	MG600390	AF261068	AF242267	KT991655	–
Rhamphoriopsis aquimicrospora	GZCC 20-0515 T	OP377812	OP377911	OP377996	OP473085	OP472992
Rhodoveronaea aquatica	GZCC 20-0447	OP377862	OP377947	OP378027	OP473107	OP473041
Rubellisphaeria abscondita	CBS 132078 T	KT991678	KT991666	KT991646	KT991657	–
Spadicoides hyalostoma	CBS 131268	KY931799	KY931827	KY931884	KY931854	–
Sporidesmiella hyalosperma	KUMCC 15-0431	MK828690	MK849841	MK828306	MN124522	MN194032
Sporidesmiella novae-zelandiae	S-1256	MK828693	MK849845	–	MN124525	MN194036
Sporidesmium aquaticivaginatum	MFLUCC 15-0624 T	KX710147	KX710142	MF077541	MF135647	MF135660
Sporidesmium guizhouense	CGMCC 3.19605 T	MK818587	MK818586	MK818588	MK828516	MK828512
Sporidesmium olivaceoconidium	MFLUCC 15-0380 T	KX710144	KX710139	MF077542	MF135648	MF135661
Thailandiomyces bisetulosus	BCC 00018	–	EF622230	EF622229	–	–
Thyridium flavostromatum	MAFF 247509 T	LC655959	LC655963	–	LC655967	LC655971
Thyridium punctulatum	MAFF 247510 T	LC655962	LC655966	–	LC655970	LC655974
Torrentispora aquatica	HKU(M) 17484	–	AY780365	–	–	–
Torrentispora fibrosa	ICMP 15147	KY931806	EF577060	KY931890	KY931859	–
Wongia aquatica	MFLUCC 18-1607 T	MK828645	MK849788	MK828312	MN124536	MN194048
Wongia flava	CGMCC 3.25434 T	OR589341	OR769700	OR743229	OR820915	OR739187
Wongia miscanthi	BCRC FU32062 T	LC822730	LC822732	LC822736	LC822734	LC822738
Wongia suae	CGMCC 3.24295 T	OQ911478	OQ911483	OQ998925	OR039047	OR039046
Woswasia atropurpurea	WU32007 T	NR_154480	JX233658	JX233658	JX233659	–
Xenodactylaria thailandica	CBS 145074 T	MK047443	MK047493	–	–	–
Xylochrysis lucida	CBS 135996 T	NR_132063	KF539911	KF539912	KF539913	–

Notes: The ex-type cultures are indicated using "T" after strain numbers; newly generated sequences are indicated in bold. A hyphen (–) stands for no sequence data in GenBank.

Results

Phylogenetic analysis

Maximum likelihood (ML) phylogenetic analysis was conducted using a concatenated dataset of LSU, SSU, *rpb*2, and *tef*1-α sequences (4,056 characters, including gaps) from 129 ingroup strains, primarily within Diaporthomycetidae. The analysis resolved a monophyletic clade comprising four monotypic genera, which clustered with Papulosaceae within Diaporthomycetidae families *incertae sedis* with 62% ML bootstrap support (Suppl. material 1: fig. S1). This clade includes *Aquimonospora tratensis* (MFLUCC 17-2133), *Multiseptisporium aquaticum* gen. et sp. nov. (KUNCC 23-14304 and GZCC 24-0036), *Paradiplococcium singulare* (FMR 10752), and *Platytrachelon abietis* (CBS 125235).

A second ML analysis based on an expanded dataset combining LSU, ITS, SSU, *rpb*2, and *tef*1-α sequences (4,056 characters, including gaps) produced a similar topology, with the same four taxa forming a monophyletic lineage sister to Papulosaceae (Fig. 1). Phylogenetic trees inferred from ML and Bayesian inference (BI) analyses were largely congruent in overall topology (Fig. 1), with *Chlorociboria aeruginosa* (AFTOL-ID 151) and *Dermea acerina* (AFTOL-ID 941) selected as outgroup taxa. In addition, phylogenetic analyses based on individual gene regions were conducted and are presented in the Supplementary Materials (Suppl. material 1: figs S2–S6).

Taxonomy

Platytrachelaceae H.W. Shen & Z.L. Luo, fam. nov.
Fungal Names: FN 573256
Chinese name: 扁喙壳科 (Pinyin: Biǎn huì ké kē)

Etymology. The family name Platytrachelaceae is derived from the type genus *Platytrachelon*.

Type genus. *Platytrachelon* Réblová, detailed description and illustrations by Réblová (2013).

Description. ***Saprobic*** on decaying wood. **Asexual morph**: Hyphomycetous. ***Mycelium*** immersed to superficial, composed of pale brown to brown, septate, branched hyphae. ***Conidiophores*** semi-macronematous to macronematous, mononematous, cylindrical, septate, unbranched, or reduced to conidiogenous cells. ***Conidiogenous cells*** enteroblastic, mono- to polyblastic, phialidic, polytretic, integrated or discrete, terminal or intercalary, cylindrical, clavate, ampulliform, spherical, sympodial, with denticulate or collarette, proliferating or non-proliferating. ***Conidia*** solitary or in short chains, hyaline to dark brown, ellipsoidal, obovoid to cylindrical, obclavate to rostrate, falcate or filiform, aseptate to multi-septate, with or without a sheath and appendages. **Sexual morph**: ***Ascomata*** immersed to superficial, subglobose to globose, dark brown to black, uniloculate. ***Necks*** central, cylindrical, ostiolate. ***Peridium*** leathery, two-layered. ***Paraphyses*** hyaline, branched, septate. ***Asci*** 8-spored, unitunicate, cylindric-clavate, long pedicellate, with an apical annulus. ***Ascospores*** uniseriate, hyaline, fusiform, septate.

Accepted genera. *Aquimonospora*, *Multiseptisporium*, *Paradiplococcium*, and *Platytrachelon*.

Notes. The new family Platytrachelaceae is proposed to accommodate *Multiseptisporium* gen. nov. and three previously monotypic genera, *Aquimonospora*, *Paradiplococcium*, and *Platytrachelon*, which were formerly placed in Diaporthomycetidae genera incertae sedis and Sordariomycetes genera

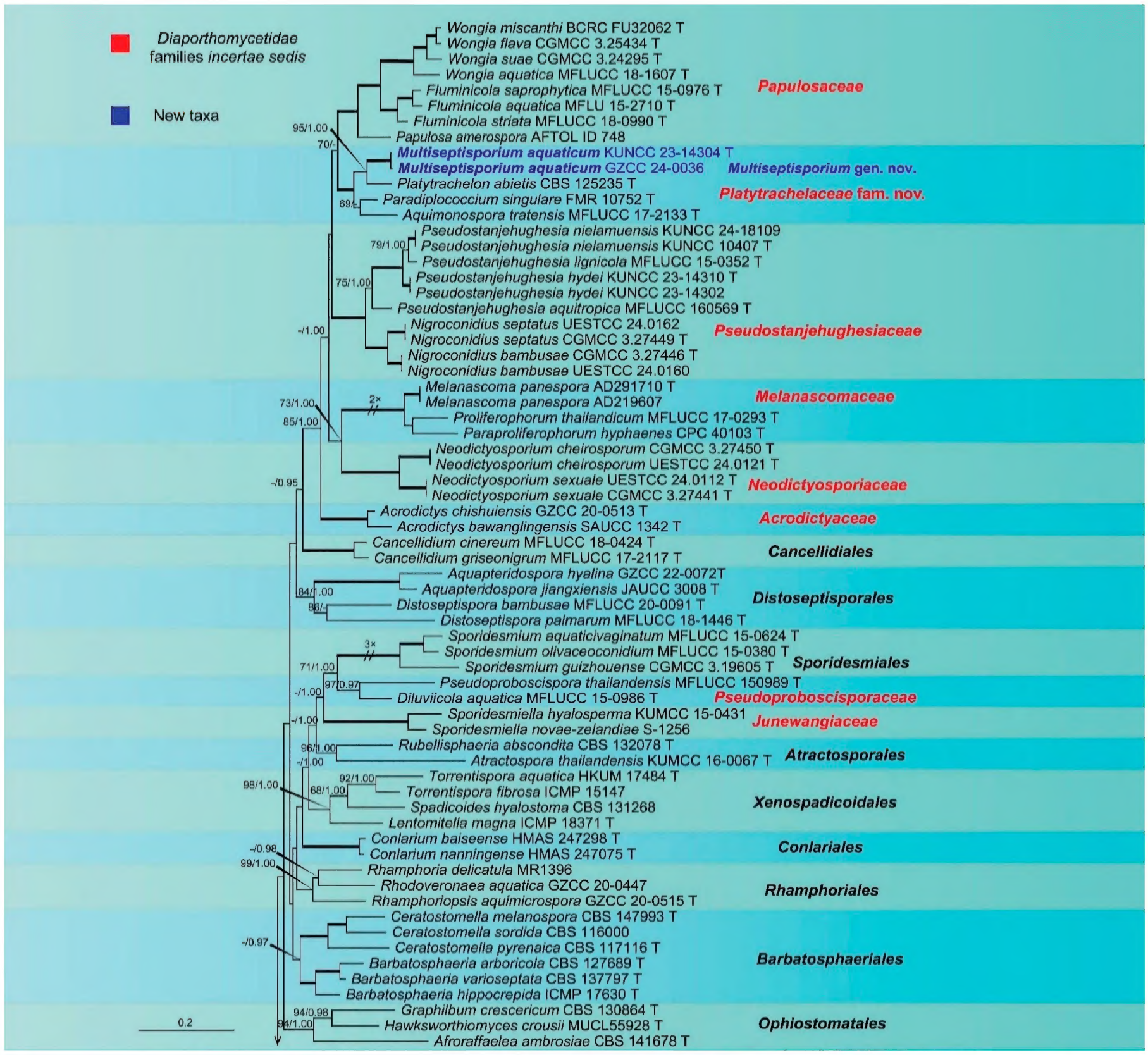

Figure 1. Phylogram generated from maximum likelihood analysis based on a combined LSU, ITS, SSU, *rpb*2, and *tef*1-α sequence dataset representing Sordariomycetes. A total of 129 strains are included in the combined analyses, comprising 4,056 characters, including gaps (753 characters for LSU, 491 characters for ITS, 1,003 characters for SSU, 953 characters for *rpb*2, and 856 characters for *tef*1-α). *Chlorociboria aeruginosa* (AFTOL-ID 151) and *Dermea acerina* (AFTOL-ID 941) were selected as the outgroup taxa. Phylogenetic trees generated from ML and BI analyses were similar in overall topology. The likelihood of the final tree was evaluated and optimized under GAMMA. The best RAxML tree with a final likelihood value of −99,500.004295 is presented. The matrix contained 2,581 distinct alignment patterns, with 26.92% undetermined characters or gaps. Estimated base frequencies were as follows: A = 0.242196, C = 0.257588, G = 0.279259, T = 0.220957; substitution rates AC = 1.228123, AG = 2.867394, AT = 1.190549, CG = 1.260961, CT = 6.459408, GT = 1.000000; α = 0.344777; tree length = 16.144614. Bayesian analyses generated 3,492 trees (average standard deviation of split frequencies = 0.009982), from which 2,620 trees were sampled after 25% were discarded as burn-in. The alignment contained a total of 2,581 unique site patterns. Bootstrap support values with ML ≥ 65% and Bayesian posterior probabilities (PP) ≥ 0.96 are given above the nodes as MLBS/BYPP. Thickened branches represent nodes with MLBS values of 100% and BYPP values of 1.00. A hyphen (–) indicates values lower than 65% MLBS or 0.95 PP. The ex-type cultures are indicated using "T" after strain numbers, and newly generated sequences are shown in bold blue.

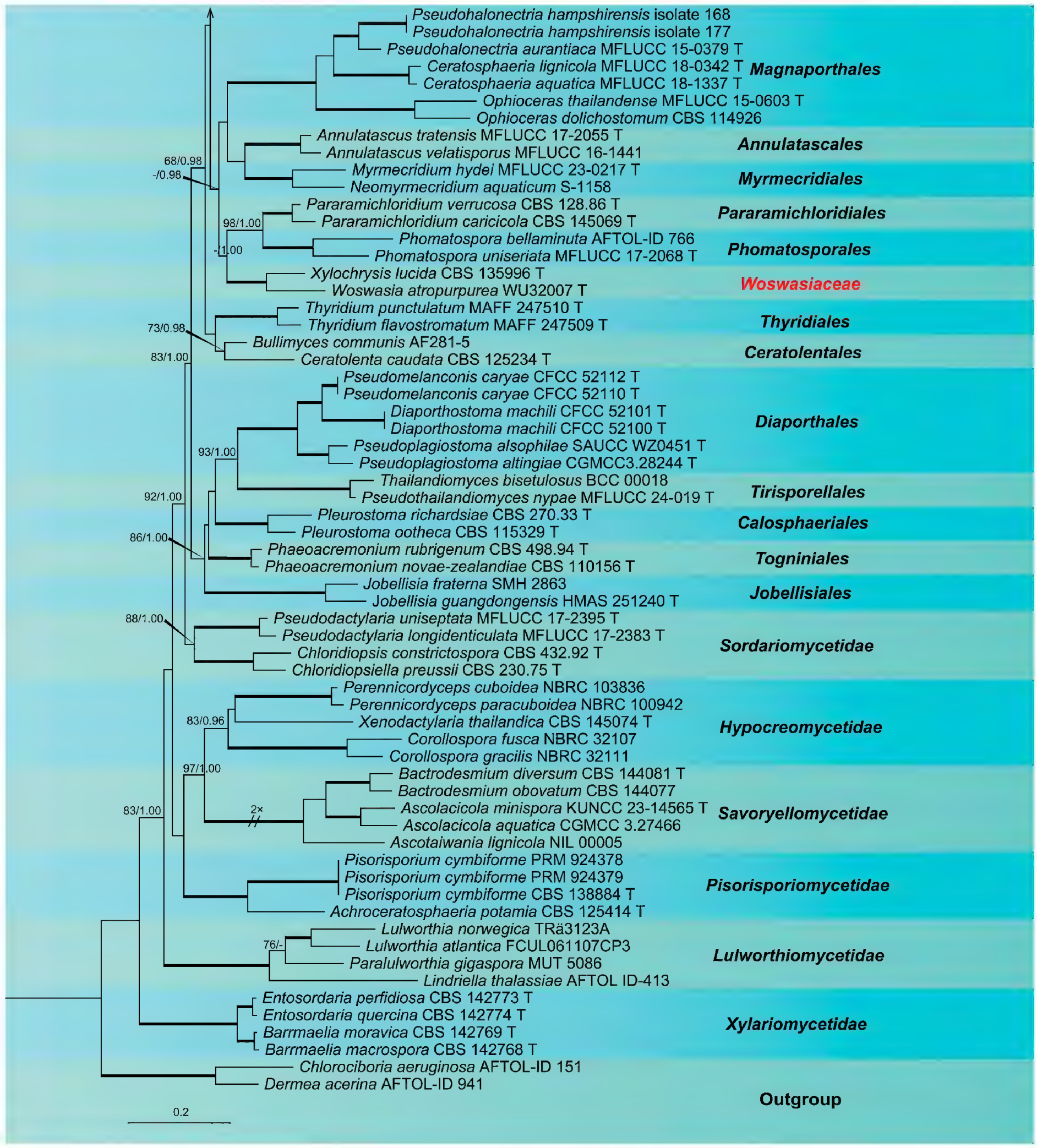

Figure 1. Continued.

incertae sedis (Hyde et al. 2024). In our multi-gene phylogenetic analyses, these four genera consistently formed an independent clade, clearly distinct from all currently recognized families within Diaporthomycetidae families *incertae sedis* (Fig. 1, Suppl. material 1: fig. S1). Consistent results were also recovered in single-gene maximum likelihood analyses, in which Platytrachelaceae repeatedly emerged as an independent lineage distinct from other families and orders within Diaporthomycetidae (Suppl. material 1: figs S2–S6). However, due to relatively low support values for the backbone of this lineage, we tentatively place it in Diaporthomycetidae families *incertae sedis*. The family is typified by the genus *Platytrachelon*, which was introduced by Réblová (2013) to accommodate *P. abietis*

(formerly *Ceratosphaeria abietis*), based on a combination of morphological characteristics and phylogenetic placement. *Platytrachelon abietis* was originally described based on its sexual morph, and subsequent studies documented its asexual morph on PCA medium, including the presence of synanamorphs (Réblová 2013). Although *Platytrachelon* remains monotypic, it is currently the only genus within Platytrachelaceae for which both sexual and asexual morphs have been documented. This morphological completeness supports the designation of *Platytrachelon* as the type genus of Platytrachelaceae.

Multiseptisporium **H.W. Shen & Z.L. Luo, gen. nov.**

Fungal Names: FN 573257

Chinese name: 多隔孢属 (Pinyin: Duō gé bāo shǔ)

Etymology. From Latin multi- (many), septum (a partition or septum), and sporium (spore), referring to the multi-septate conidia of the genus.

Type species. *Multiseptisporium aquaticum* H.W. Shen & Z.L. Luo, sp. nov.

Description. ***Saprobic*** on submerged decaying wood. **Sexual morph**: Undetermined. **Asexual morph**: ***Colonies*** on natural substrate, effuse, scattered, superficial, hairy, dark brown. ***Mycelium*** partly immersed and partly superficial. ***Conidiophores*** macronematous, mononematous, cylindrical, septate, unbranched. ***Conidiogenous cells*** monoblastic, integrated, terminal, cylindrical, sometimes percurrently proliferating. ***Conidial secession*** rhexolytic. ***Conidia*** acrogenous, solitary, obclavate to rostrate, truncated at the base, brown to dark brown, euseptate, guttulate, smooth, occasionally verruculous, with a light-colored, truncated, cuneiform basal cell and a subhyaline, acuminate apical cell, with or without sheath and appendages.

Notes. Multi-gene phylogenetic analyses revealed that the two collections of *Multiseptisporium* formed a distinct monophyletic clade that clustered with three monotypic genera, *Aquimonospora*, *Paradiplococcium*, and *Platytrachelon*, within Diaporthomycetidae genera incertae sedis and Sordariomycetes genera *incertae sedis* (Hyde et al. 2024; Fig. 1, Suppl. material 1: fig. S1). *Multiseptisporium* from these genera by producing a sporidesmium-like asexual morph, whereas its sexual morph remains undetermined. In contrast, *Aquimonospora* produces clavate, obovoid, or fusiform, septate conidia arising from integrated, terminal, monoblastic, enteroblastic conidiogenous cells (Yang et al. 2019). *Paradiplococcium* is characterized by subcylindrical to obovoid conidia in short chains and derived from polytretic, integrated or discrete, terminal or intercalary conidiogenous cells (Hernández-Restrepo et al. 2011). In culture, *Paradiplococcium* also produces a synanamorph with hyaline, falcate to filiform conidia developed from polyblastic, sympodial, denticulate conidiogenous cells (Hernández-Restrepo et al. 2011). *Platytrachelon* is known to produce both sexual and asexual morphs. Its asexual morph has been observed on PCA medium, where ellipsoidal, septate conidia are produced either directly from hyphae or from blastic, sympodial conidiogenous cells (Réblová 2013). Additionally, synanamorphic conidia are produced from blastic, phialidic conidiogenous cells. The clear morphological distinctions among these genera, combined with their phylogenetic relationships, support the recognition of *Multiseptisporium* as a novel genus.

Multiseptisporium aquaticum **H.W. Shen & Z.L. Luo, sp. nov.**

Fungal Names: FN 573258

Fig. 2

Chinese name: 水生多隔孢 (Pinyin: Shuǐ shēng duō gé bāo)

Etymology. The specific epithet "*aquaticum*" refers to the aquatic habitat where the fungus was collected.

Holotype. HKAS 151655.

Description. ***Saprobic*** on submerged decaying wood in freshwater habitats. **Sexual morph**: Undetermined. **Asexual morph**: ***Colonies*** on natural substrate, superficial, effuse, scattered, hairy, dark brown, solitary, or in small groups of 2–3. ***Mycelium*** partly immersed and partly superficial, composed of branched, septate, brown to dark brown, smooth-walled hyphae. ***Conidiophores*** (104–)120–204(–234) × 6–8 μm ($\bar{x}$ = 162 × 7 μm, SD = 41.6 × 0.6, n = 15), macronematous, mononematous, cylindrical, straight or slightly flexuous, unbranched, 8–9-septate, slightly enlarged at the base, dark brown to black, smooth-walled. ***Conidiogenous cells*** (11–)14–21(–23) × 4–6 μm ($\bar{x}$ = 18 × 5 μm, SD = 3.0 × 0.5, n = 15), monoblastic, integrated, terminal, determinate, cylindrical, slightly narrow at the top, brown, smooth-walled. ***Conidial secession*** rhexolytic. ***Conidia*** (53–)57–68(–75) × 10–14 μm ($\bar{x}$ = 63 × 12 μm, SD = 5.7 × 1.2, n = 15), acrogenous, solitary, straight to slightly curved, 8–10-euseptate, obclavate to rostrate, truncated at base, tapering towards an acuminate apex, brown to dark olivaceous brown, subhyaline at apex, typically widest at third cell from base, with cuneiform basal cell, similar in color to apical cells, slightly constricted at septa, guttulate, smooth, occasionally verruculous, sometimes with an inconspicuous sheath at apex.

Culture characteristics. Conidia germinating on PDA within 12 h and germ tubes produced from both ends. Colonies on PDA reaching 2–3 cm in diameter after two months at room temperature (around 22 °C) in the dark, dense, velvety, gray to dark brown at the margins, pale to gray at the center, with irregular margins and bulge center from above; dense, gray to dark gray, with irregular margins from below.

Material examined. China • Yunnan Province, Honghe Hani and Yi Autonomous Prefecture, Shiping County, Yilonghu Lake, 23°40'56.4"N, 101°43'46.8"E, elevation 1400 m, on the unknown submerged decaying wood, 23 February 2023, H.W. Shen, L2194 (HKAS 151655, holotype), ex-type KUNCC 23-14304; • ibid. Guizhou Province, Zunyi City, Xishui County, 28°9'17"N, 105°55'50"E, elevation 640 m, on the unknown submerged decaying wood, 2 October 2023, X.J. Xiao, NJS15 (HKAS 152855, paratype), ex-paratype GZCC 24-0036.

Notes. Phylogenetic analysis revealed that *Multiseptisporium aquaticum* (KUNCC 23-14304 and GZCC 24-0036) clustered with *Platytrachelon abietis* (CBS 125235) with stable support (Fig. 1). *Platytrachelon abietis*, originally described as *Ceratosphaeria abietis*, was collected from the inner side of decaying bark of *Abies alba* in the Czech Republic and has also been reported from Ukraine (Réblová 2013). Based on morphological and phylogenetic evidence, Réblová (2013) transferred *C. abietis* to the newly established genus *Platytrachelon*. Both sexual and asexual morphs of *P. abietis* have been documented. Notably, the asexual morph, including a synanamorph, was observed on PCA culture media. The asexual form of *P. abietis* is characterized by spherical, hyaline to

Figure 2. *Multiseptisporium aquaticum* (HKAS 151655, holotype). **a, b.** Colonies on woody substrates; **c–e.** Conidiophores with conidia; **f.** Conidiogenous cell; **g.** Conidiogenous cell with conidia; **h, i.** Conidia; **j.** Germinated conidium; **k.** Culture on PDA, upper surface and reverse. Scale bars: 40 μm (**c–e**); 15 μm (**f, g**); 20 μm (**h–j**).

subhyaline, holoblastic conidiogenous cells that proliferate sympodially; ellipsoidal, septate, smooth-walled conidia, sometimes arising directly from subhyaline or pigmented hyphae. The synanamorph is characterized by cylindrical to ampulliform, one-celled, hyaline to subhyaline conidiogenous cells terminating in a single phialidic opening or with an additional lateral opening; the collarette is shallow, wedge-shaped, and inconspicuous; conidia are cylindrical, strongly curved, hyaline, one-celled, and smooth-walled (Réblová 2013). *Multiseptisporium aquaticum* differs from *P. abietis* in having sporidesmium-like conidia produced from monoblastic, terminal, cylindrical conidiogenous cells, with rhexolytic conidial secession. No synanamorphs were observed. Comparison of nucleotide base differences in LSU and *rpb*2 sequence data between *M. aquaticum* (KUNCC 23-14304) and *P. abietis* (CBS 125235) showed differences of 3.2% (34/1,071 bp, including four gaps) and 11.8% (122/1,032 bp), respectively. Based on the combined morphological characteristics and sequence data, *M. aquaticum* is proposed as a new species.

Discussion

Phylogenetic analyses revealed that four monotypic genera, *Aquimonospora*, *Multiseptisporium*, *Paradiplococcium*, and *Platytrachelon*, clustered within a well-supported monophyletic lineage related to Papulosaceae, Pseudostanjehughesiaceae, Melanascomaceae, and Neodictyosporiaceae in Diaporthomycetidae families *incertae sedis* (Hyde et al. 2024; Yu et al. 2024; Fig. 1, Suppl. material 1: fig. S1). The earliest described species within this lineage, *Platytrachelon abietis*, was initially assigned to Papulosaceae based on morphological and phylogenetic evidence (Réblová 2013). However, subsequent studies indicated that it does not belong to Papulosaceae, and it has since been treated as a member of Diaporthomycetidae genera *incertae sedis* (Réblová et al. 2016, 2018; Luo et al. 2019; Yang et al. 2019; Hyde et al. 2024). Based on morphological distinctiveness, such as discrete conidiogenous cells and short chains of conidia, and phylogenetic analyses of combined LSU and SSU sequences, *Paradiplococcium singulare*, originally described as *Diplococcium singulare* and later transferred to the monotypic genus *Paradiplococcium* by Hernandez-Restrepo et al. (2017), was subsequently placed in Sordariomycetes incertae sedis. *Aquimonospora tratensis* was established by Yang et al. (2019) from submerged woody substrates in freshwater habitats in Thailand. Its conidia are clavate, obovoid, or fusiform and composed of two parts: an upper part with brown to dark brown conidial cells and a lower part of two subhyaline to pale brown cells. Phylogenetic analyses showed that *A. tratensis* is closely related to *P. abietis* and belongs to the Diaporthomycetidae genera *incertae sedis* (Yang et al. 2019). Our multi-gene phylogenetic analyses, based on combined LSU, ITS, SSU, *rpb*2, and *tef*1-α datasets, yielded results consistent with those of Yang et al. (2019), showing that these four monotypic genera form a distinct and strongly supported clade related to Papulosaceae. Based on these results, a new family, Platytrachelaceae, is proposed to accommodate these four genera within the Diaporthomycetidae families *incertae sedis*.

Paradiplococcium singulare and *P. abietis* have been examined from both natural materials and artificial cultures, where they produced asexual morphs and synanamorphs on PCA and OA media (Réblová 2013; Hernandez-Restrepo et al.

2017). In contrast, *A. tratensis* and *M. aquaticum* are known only from natural substrates, with no asexual morphs observed in culture. Notably, *Pa. singulare* and *P. abietis* readily sporulate on PCA and OA media, suggesting that these media may promote conidial development in this lineage and related taxa (Réblová 2013; Hernandez-Restrepo et al. 2017; Crous et al. 2019; Réblová and Nekvindová 2023). We plan to culture our isolates on PCA and OA media to induce sporulation and obtain additional morphological characteristics that may provide further insights into their taxonomy (Su et al. 2012; Liao et al. 2025). The induction of sporulation in culture and the subsequent characterization of cultural morphs represent essential approaches for studying fungal diversity. Such methods are not only valuable for endophytic fungi but also play a crucial role in the investigation of saprobic taxa (Crous et al. 2019; Réblová et al. 2021; Réblová and Nekvindová 2023; Liao et al. 2025). Compared with morphological features observed on natural substrates, sporulation in culture often reveals diagnostic characteristics that are consistent with those on natural substrates and are critical for accurate species and genus delimitation (Réblová 2013; Hernandez-Restrepo et al. 2017).

Sporidesmium-like taxa are phylogenetically diverse, occurring predominantly in Sordariomycetes and Dothideomycetes, with a few representatives also reported from Leotiomycetes (Shenoy et al. 2006; Su et al. 2016; Liu et al. 2024). This group is morphologically complex, exhibiting a wide range of conidiophore structures—solitary or fasciculate, dematiaceous, septate, branched or unbranched—and often percurrently proliferating from cut ends; conidiogenous cells mono- or polyblastic; and conidia obclavate to rostrate, eu- to distoseptate, with or without gelatinous sheaths or appendages (Shenoy et al. 2006; Su et al. 2016; Zhang et al. 2022; Delgado et al. 2024). However, these morphological features have proven phylogenetically unreliable for generic delimitation, and in the absence of molecular data, species assignment based solely on morphology remains problematic (Shenoy et al. 2006; Su et al. 2016; Zhang et al. 2022; Delgado et al. 2024). With the increasing application of culture-dependent studies and multi-gene phylogenetic analyses, more robust insights into the classification and evolution of sporidesmium-like taxa have been achieved (Su et al. 2016; Wu and Diao 2022; Zhang et al. 2022; Delgado et al. 2024; Tang et al. 2024). In the present study, a new sporidesmium-like genus, *Multiseptisporium*, is introduced to accommodate a novel freshwater species, *M. aquaticum*, collected from China. Morphologically, *M. aquaticum* resembles *Sporidesmium* species in having macronematous, mononematous, cylindrical, septate conidiophores; monoblastic, cylindrical, integrated conidiogenous cells; and acrogenous, solitary, obclavate to rostrate, euseptate, guttulate conidia with or without a sheath (Shenoy et al. 2006; Su et al. 2016; Liu et al. 2024). However, phylogenetic analyses based on combined LSU, ITS, SSU, *rpb*2, and *tef*1-α datasets clearly separate *M. aquaticum* from other sporidesmium-like genera within Sordariomycetes, such as *Distoseptispora* (Distoseptisporales) and *Sporidesmium* (Sporidesmiales) (Fig. 1, Suppl. material 1: fig. S1). Accordingly, *Multiseptisporium* is proposed as a new genus based on its distinct phylogenetic position.

Species within Platytrachelaceae appear to be relatively rare, as all four currently recognized genera are monotypic and exhibit distinct ecological preferences and geographical distributions. *A. tratensis* is known solely from a single collection on submerged decaying wood in a freshwater habitat in Thailand, suggesting a narrow ecological amplitude and possible specialization to tropical

freshwater woody substrates (Yang et al. 2019). *Multiseptisporium aquaticum* has been recorded from submerged woody substrates in a lake in Yunnan Province and a stream in Guizhou Province, China, indicating an aquatic lignicolous lifestyle with a degree of ecological flexibility. In contrast, *Pa. singulare* was collected from decaying wood of unknown origin in Spain, whereas *P. abietis* appears to be consistently associated with the inner bark of *Abies alba* in temperate regions of Europe, suggesting strong substrate specificity (Réblová 2013; Hernandez-Restrepo et al. 2017). The occurrence of multiple monotypic genera within Platytrachelaceae likely reflects pronounced ecological differentiation among lineages, particularly with respect to habitat type and substrate preference. Such ecological specialization may constrain species diversification within individual lineages, resulting in phylogenetically distinct but species-poor taxa. Nevertheless, given the limited number of collections currently available for most members of the family, especially microfungi from freshwater environments, expanded sampling across a broader range of habitats and geographic regions may reveal additional diversity within Platytrachelaceae.

Exploration of regional fungal diversity remains essential for understanding global mycobiota. Ongoing studies on lignicolous freshwater fungi in southwestern China have yielded several novel taxa, including *M. aquaticum*, as described herein (Luo et al. 2019; Dong et al. 2020; Bao et al. 2021; Shen et al. 2022b, 2024a; Wang et al. 2024b; Xu et al. 2025b). These findings enrich knowledge of fungal diversity in the region and contribute insights into phylogenetic relationships and distribution patterns, providing a foundation for further studies in fungal taxonomy and systematics.

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Additional information

Conflict of interest

The authors have declared that no competing interests exist.

Ethical statement

No ethical statement was reported.

Use of AI

No use of AI was reported.

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Author contributions

Formal analysis: HWS. Funding acquisition: ZLL. Investigation: HWS, DFB, XJX. Methodology: XJX, HWS. Resources: XJX. Supervision: ZLL. Writing – original draft: HWS. Writing – review and editing: JDB, XJX, YZL, ZLL, DFB.

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Data availability

All of the data that support the findings of this study are available in the main text or Supplementary Information.

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Supplementary material 1

Phylogenetic trees

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Data type: docx

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